

SEQUENCE LISTING

<110> Odyssey Thera, Inc.
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<120> PROTEIN FRAGMENT COMPLEMENTATION ASSAYS FOR HIGH-THROUGHPUT AND
 HIGH-CONTENT SCREENING

<130> ODDY006

<150> US60/445,225
 <151> 2003-02-06

<150> US10/353,090
 <151> 2003-01-29

<150> US10/154,758
 <151> 2002-05-24

<150> US09/499,464
 <151> 2000-02-07

<150> US09/017,412
 <151> 1998-02-02

<160> 31

<170> PatentIn version 3.2

<210> 1
 <211> 10
 <212> PRT
 <213> Artificial

<220>
 <223> synthetic construct, a flexible linker

<400> 1

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
 1 5 10

<210> 2
 <211> 483
 <212> DNA
 <213> Artificial

<220>
 <223> synthetic construct; RLuc(F1) with stop codon added at end

<220>
 <221> CDS
 <222> (1)..(483)
 <223> RLuc(F1) corresponds to a.a. residues 1-160 of wild-type R.
 Luciferase

```

<400>  2
atg gct tcc aag gtg tac gac ccc gag caa cgc aaa cgc atg atc act      48
Met Ala Ser Lys Val Tyr Asp Pro Glu Gln Arg Lys Arg Met Ile Thr
1          5          10          15

ggg cct cag tgg tgg gct cgc tgc aag caa atg aac gtg ctg gac tcc      96
Gly Pro Gln Trp Trp Ala Arg Cys Lys Gln Met Asn Val Leu Asp Ser
          20          25          30

ttc atc aac tac tat gat tcc gag aag cac gcc gag aac gcc gtg att     144
Phe Ile Asn Tyr Tyr Asp Ser Glu Lys His Ala Glu Asn Ala Val Ile
          35          40          45

ttt ctg cat ggt aac gct gcc tcc agc tac ctg tgg agg cac gtc gtg     192
Phe Leu His Gly Asn Ala Ala Ser Ser Tyr Leu Trp Arg His Val Val
          50          55          60

cct cac atc gag ccc gtg gct aga tgc atc atc cct gat ctg atc gga     240
Pro His Ile Glu Pro Val Ala Arg Cys Ile Ile Pro Asp Leu Ile Gly
        65          70          75          80

atg ggt aag tcc ggc aag agc ggg aat ggc tca tat cgc ctc ctg gat     288
Met Gly Lys Ser Gly Lys Ser Gly Asn Gly Ser Tyr Arg Leu Leu Asp
          85          90          95

cac tac aag tac ctc acc gct tgg ttc gag ctg ctg aac ctt cca aag     336
His Tyr Lys Tyr Leu Thr Ala Trp Phe Glu Leu Leu Asn Leu Pro Lys
          100          105          110

aaa atc atc ttt gtg ggc cac gac tgg ggg gct tgt ctg gcc ttt cac     384
Lys Ile Ile Phe Val Gly His Asp Trp Gly Ala Cys Leu Ala Phe His
          115          120          125

tac tcc tac gag cac caa gac aag atc aag gcc atc gtc cat gct gag     432
Tyr Ser Tyr Glu His Gln Asp Lys Ile Lys Ala Ile Val His Ala Glu
          130          135          140

agt gtc gtg gac gtg atc gag tcc tgg gac gag tgg cct gac atc gag     480
Ser Val Val Asp Val Ile Glu Ser Trp Asp Glu Trp Pro Asp Ile Glu
        145          150          155          160

taa                                                                    483
  
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<210> 3
 <211> 160
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

<400> 3

Met Ala Ser Lys Val Tyr Asp Pro Glu Gln Arg Lys Arg Met Ile Thr
 1 5 10 15

Gly Pro Gln Trp Trp Ala Arg Cys Lys Gln Met Asn Val Leu Asp Ser
 20 25 30

Phe Ile Asn Tyr Tyr Asp Ser Glu Lys His Ala Glu Asn Ala Val Ile
 35 40 45

Phe Leu His Gly Asn Ala Ala Ser Ser Tyr Leu Trp Arg His Val Val
 50 55 60

Pro His Ile Glu Pro Val Ala Arg Cys Ile Ile Pro Asp Leu Ile Gly
 65 70 75 80

Met Gly Lys Ser Gly Lys Ser Gly Asn Gly Ser Tyr Arg Leu Leu Asp
 85 90 95

His Tyr Lys Tyr Leu Thr Ala Trp Phe Glu Leu Leu Asn Leu Pro Lys
 100 105 110

Lys Ile Ile Phe Val Gly His Asp Trp Gly Ala Cys Leu Ala Phe His
 115 120 125

Tyr Ser Tyr Glu His Gln Asp Lys Ile Lys Ala Ile Val His Ala Glu
 130 135 140

Ser Val Val Asp Val Ile Glu Ser Trp Asp Glu Trp Pro Asp Ile Glu
 145 150 155 160

<210> 4
 <211> 480
 <212> DNA
 <213> Artificial

<220>
 <223> synthetic construct; RLuc(F1) with stop codon added at end and
 initial "atg" (or Met) removed

<220>
 <221> CDS
 <222> (1)..(480)
 <223> RLuc(F1) corresponds to a.a. residues 1-160 of wild-type R.
 Luciferase

<400> 4

gct tcc aag gtg tac gac ccc gag caa cgc aaa cgc atg atc act ggg	48
Ala Ser Lys Val Tyr Asp Pro Glu Gln Arg Lys Arg Met Ile Thr Gly	
1 5 10 15	
cct cag tgg tgg gct cgc tgc aag caa atg aac gtg ctg gac tcc ttc	96
Pro Gln Trp Trp Ala Arg Cys Lys Gln Met Asn Val Leu Asp Ser Phe	
20 25 30	
atc aac tac tat gat tcc gag aag cac gcc gag aac gcc gtg att ttt	144
Ile Asn Tyr Tyr Asp Ser Glu Lys His Ala Glu Asn Ala Val Ile Phe	
35 40 45	
ctg cat ggt aac gct gcc tcc agc tac ctg tgg agg cac gtc gtg cct	192
Leu His Gly Asn Ala Ala Ser Ser Tyr Leu Trp Arg His Val Val Pro	
50 55 60	
cac atc gag ccc gtg gct aga tgc atc atc cct gat ctg atc gga atg	240
His Ile Glu Pro Val Ala Arg Cys Ile Ile Pro Asp Leu Ile Gly Met	
65 70 75 80	
ggt aag tcc ggc aag agc ggg aat ggc tca tat cgc ctc ctg gat cac	288
Gly Lys Ser Gly Lys Ser Gly Asn Gly Ser Tyr Arg Leu Leu Asp His	
85 90 95	
tac aag tac ctc acc gct tgg ttc gag ctg ctg aac ctt cca aag aaa	336
Tyr Lys Tyr Leu Thr Ala Trp Phe Glu Leu Leu Asn Leu Pro Lys Lys	
100 105 110	
atc atc ttt gtg ggc cac gac tgg ggg gct tgt ctg gcc ttt cac tac	384
Ile Ile Phe Val Gly His Asp Trp Gly Ala Cys Leu Ala Phe His Tyr	
115 120 125	
tcc tac gag cac caa gac aag atc aag gcc atc gtc cat gct gag agt	432
Ser Tyr Glu His Gln Asp Lys Ile Lys Ala Ile Val His Ala Glu Ser	
130 135 140	
gtc gtg gac gtg atc gag tcc tgg gac gag tgg cct gac atc gag taa	480
Val Val Asp Val Ile Glu Ser Trp Asp Glu Trp Pro Asp Ile Glu	
145 150 155	

<210> 5
<211> 159
<212> PRT
<213> Artificial

<220>
<223> Synthetic Construct

<400> 5

Ala Ser Lys Val Tyr Asp Pro Glu Gln Arg Lys Arg Met Ile Thr Gly
1 5 10 15

Pro Gln Trp Trp Ala Arg Cys Lys Gln Met Asn Val Leu Asp Ser Phe
20 25 30

Ile Asn Tyr Tyr Asp Ser Glu Lys His Ala Glu Asn Ala Val Ile Phe
35 40 45

Leu His Gly Asn Ala Ala Ser Ser Tyr Leu Trp Arg His Val Val Pro
50 55 60

His Ile Glu Pro Val Ala Arg Cys Ile Ile Pro Asp Leu Ile Gly Met
65 70 75 80

Gly Lys Ser Gly Lys Ser Gly Asn Gly Ser Tyr Arg Leu Leu Asp His
85 90 95

Tyr Lys Tyr Leu Thr Ala Trp Phe Glu Leu Leu Asn Leu Pro Lys Lys
100 105 110

Ile Ile Phe Val Gly His Asp Trp Gly Ala Cys Leu Ala Phe His Tyr
115 120 125

Ser Tyr Glu His Gln Asp Lys Ile Lys Ala Ile Val His Ala Glu Ser
130 135 140

Val Val Asp Val Ile Glu Ser Trp Asp Glu Trp Pro Asp Ile Glu
145 150 155

<210> 6
 <211> 459
 <212> DNA
 <213> Artificial

<220>

<223> synthetic construct; RLuc(F2) an "atg" (or Met) has been added at position 1 and a stop codon added at the end of the fragment

<220>

<221> CDS

<222> (1)..(459)

<223> RLuc(F2) corresponds to a.a. residues 161-311 of wild-type R. Luciferase

<400> 6

atg gag gat atc gcc ctg atc aag agc gaa gag ggc gag aaa atg gtg	48
Met Glu Asp Ile Ala Leu Ile Lys Ser Glu Gly Glu Lys Met Val	
1 5 10 15	
ctt gag aat aac ttc ttc gtc gag acc atg ctc cca agc aag atc atg	96
Leu Glu Asn Asn Phe Phe Val Glu Thr Met Leu Pro Ser Lys Ile Met	
20 25 30	
cgg aaa ctg gag cct gag gag ttc gct gcc tac ctg gag cca ttc aag	144
Arg Lys Leu Glu Pro Glu Glu Phe Ala Ala Tyr Leu Glu Pro Phe Lys	
35 40 45	
gag aag ggc gag gtt aga cgg cct acc ctc tcc tgg cct cgc gag atc	192
Glu Lys Gly Glu Val Arg Arg Pro Thr Leu Ser Trp Pro Arg Glu Ile	
50 55 60	
cct ctc gtt aag gga ggc aag ccc gac gtc gtc cag att gtc cgc aac	240
Pro Leu Val Lys Gly Gly Lys Pro Asp Val Val Gln Ile Val Arg Asn	
65 70 75 80	
tac aac gcc tac ctt cgg gcc agc gac gat ctg cct aag atg ttc atc	288
Tyr Asn Ala Tyr Leu Arg Ala Ser Asp Asp Leu Pro Lys Met Phe Ile	
85 90 95	
gag tcc gac cct ggg ttc ttt tcc aac gct att gtc gag gga gct aag	336
Glu Ser Asp Pro Gly Phe Phe Ser Asn Ala Ile Val Glu Gly Ala Lys	
100 105 110	
aag ttc cct aac acc gag ttc gtg aag gtg aag ggc ctc cac ttc agc	384
Lys Phe Pro Asn Thr Glu Phe Val Lys Val Lys Gly Leu His Phe Ser	
115 120 125	
cag gag gac gct cca gat gaa atg ggt aag tac atc aag agc ttc gtg	432
Gln Glu Asp Ala Pro Asp Glu Met Gly Lys Tyr Ile Lys Ser Phe Val	
130 135 140	
gag cgc gtg ctg aag aac gag cag taa	459
Glu Arg Val Leu Lys Asn Glu Gln	
145 150	

<210> 7
 <211> 152
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

<400> 7

Met Glu Asp Ile Ala Leu Ile Lys Ser Glu Glu Gly Glu Lys Met Val
 1 5 10 15

Leu Glu Asn Asn Phe Phe Val Glu Thr Met Leu Pro Ser Lys Ile Met
 20 25 30

Arg Lys Leu Glu Pro Glu Glu Phe Ala Ala Tyr Leu Glu Pro Phe Lys
 35 40 45

Glu Lys Gly Glu Val Arg Arg Pro Thr Leu Ser Trp Pro Arg Glu Ile
 50 55 60

Pro Leu Val Lys Gly Gly Lys Pro Asp Val Val Gln Ile Val Arg Asn
 65 70 75 80

Tyr Asn Ala Tyr Leu Arg Ala Ser Asp Asp Leu Pro Lys Met Phe Ile
 85 90 95

Glu Ser Asp Pro Gly Phe Phe Ser Asn Ala Ile Val Glu Gly Ala Lys
 100 105 110

Lys Phe Pro Asn Thr Glu Phe Val Lys Val Lys Gly Leu His Phe Ser
 115 120 125

Gln Glu Asp Ala Pro Asp Glu Met Gly Lys Tyr Ile Lys Ser Phe Val
 130 135 140

Glu Arg Val Leu Lys Asn Glu Gln
 145 150

<210> 8
 <211> 456
 <212> DNA
 <213> Artificial

 <220>
 <223> synthetic construct; RLuc(F2) with a stop codon added at the end of the fragment

 <220>
 <221> CDS

 <222> (1)..(456)
 <223> RLuc(F2) corresponds to a.a. residues 161-311 of wild-type R. Luciferase

 <400> 8
 gag gat atc gcc ctg atc aag agc gaa gag ggc gag aaa atg gtg ctt 48
 Glu Asp Ile Ala Leu Ile Lys Ser Glu Glu Gly Glu Lys Met Val Leu
 1 5 10 15

 gag aat aac ttc ttc gtc gag acc atg ctc cca agc aag atc atg cgg 96
 Glu Asn Asn Phe Phe Val Glu Thr Met Leu Pro Ser Lys Ile Met Arg
 20 25 30

 aaa ctg gag cct gag gag ttc gct gcc tac ctg gag cca ttc aag gag 144
 Lys Leu Glu Pro Glu Glu Phe Ala Ala Tyr Leu Glu Pro Phe Lys Glu
 35 40 45

 aag ggc gag gtt aga cgg cct acc ctc tcc tgg cct cgc gag atc cct 192
 Lys Gly Glu Val Arg Arg Pro Thr Leu Ser Trp Pro Arg Glu Ile Pro
 50 55 60

 ctc gtt aag gga ggc aag ccc gac gtc gtc cag att gtc cgc aac tac 240
 Leu Val Lys Gly Gly Lys Pro Asp Val Val Gln Ile Val Arg Asn Tyr
 65 70 75 80

 aac gcc tac ctt cgg gcc agc gac gat ctg cct aag atg ttc atc gag 288
 Asn Ala Tyr Leu Arg Ala Ser Asp Asp Leu Pro Lys Met Phe Ile Glu
 85 90 95

 tcc gac cct ggg ttc ttt tcc aac gct att gtc gag gga gct aag aag 336
 Ser Asp Pro Gly Phe Phe Ser Asn Ala Ile Val Glu Gly Ala Lys Lys
 100 105 110

 ttc cct aac acc gag ttc gtg aag gtg aag ggc ctc cac ttc agc cag 384
 Phe Pro Asn Thr Glu Phe Val Lys Val Lys Gly Leu His Phe Ser Gln
 115 120 125

 gag gac gct cca gat gaa atg ggt aag tac atc aag agc ttc gtg gag 432
 Glu Asp Ala Pro Asp Glu Met Gly Lys Tyr Ile Lys Ser Phe Val Glu
 130 135 140

 cgc gtg ctg aag aac gag cag taa 456
 Arg Val Leu Lys Asn Glu Gln

145

150

<210> 9

<211> 151

<212> PRT

<213> Artificial

<220>

<223> Synthetic Construct

<400> 9

Glu Asp Ile Ala Leu Ile Lys Ser Glu Glu Gly Glu Lys Met Val Leu
1 5 10 15

Glu Asn Asn Phe Phe Val Glu Thr Met Leu Pro Ser Lys Ile Met Arg
20 25 30

Lys Leu Glu Pro Glu Glu Phe Ala Ala Tyr Leu Glu Pro Phe Lys Glu
35 40 45

Lys Gly Glu Val Arg Arg Pro Thr Leu Ser Trp Pro Arg Glu Ile Pro
50 55 60

Leu Val Lys Gly Gly Lys Pro Asp Val Val Gln Ile Val Arg Asn Tyr
65 70 75 80

Asn Ala Tyr Leu Arg Ala Ser Asp Asp Leu Pro Lys Met Phe Ile Glu
85 90 95

Ser Asp Pro Gly Phe Phe Ser Asn Ala Ile Val Glu Gly Ala Lys Lys
100 105 110

Phe Pro Asn Thr Glu Phe Val Lys Val Lys Gly Leu His Phe Ser Gln
115 120 125

Glu Asp Ala Pro Asp Glu Met Gly Lys Tyr Ile Lys Ser Phe Val Glu
130 135 140

Arg Val Leu Lys Asn Glu Gln
145 150

<210> 10
 <211> 483
 <212> DNA
 <213> Artificial

<220>

<223> synthetic construct; RLuc(F1) with a C124A mutation and stop codon at end

<220>

<221> CDS

<222> (1)..(483)

<400> 10

atg gct tcc aag gtg tac gac ccc gag caa cgc aaa cgc atg atc act	48
Met Ala Ser Lys Val Tyr Asp Pro Glu Gln Arg Lys Arg Met Ile Thr	
1 5 10 15	

ggg cct cag tgg tgg gct cgc tgc aag caa atg aac gtg ctg gac tcc	96
Gly Pro Gln Trp Trp Ala Arg Cys Lys Gln Met Asn Val Leu Asp Ser	
20 25 30	

ttc atc aac tac tat gat tcc gag aag cac gcc gag aac gcc gtg att	144
Phe Ile Asn Tyr Tyr Asp Ser Glu Lys His Ala Glu Asn Ala Val Ile	
35 40 45	

ttt ctg cat ggt aac gct gcc tcc agc tac ctg tgg agg cac gtc gtg	192
Phe Leu His Gly Asn Ala Ala Ser Ser Tyr Leu Trp Arg His Val Val	
50 55 60	

cct cac atc gag ccc gtg gct aga tgc atc atc cct gat ctg atc gga	240
Pro His Ile Glu Pro Val Ala Arg Cys Ile Ile Pro Asp Leu Ile Gly	
65 70 75 80	

atg ggt aag tcc ggc aag agc ggg aat ggc tca tat cgc ctc ctg gat	288
Met Gly Lys Ser Gly Lys Ser Gly Asn Gly Ser Tyr Arg Leu Leu Asp	
85 90 95	

cac tac aag tac ctc acc gct tgg ttc gag ctg ctg aac ctt cca aag	336
His Tyr Lys Tyr Leu Thr Ala Trp Phe Glu Leu Leu Asn Leu Pro Lys	
100 105 110	

aaa atc atc ttt gtg ggc cac gac tgg ggg gct gct ctg gcc ttt cac	384
Lys Ile Ile Phe Val Gly His Asp Trp Gly Ala Ala Leu Ala Phe His	
115 120 125	

tac tcc tac gag cac caa gac aag atc aag gcc atc gtc cat gct gag	432
Tyr Ser Tyr Glu His Gln Asp Lys Ile Lys Ala Ile Val His Ala Glu	
130 135 140	

agt gtc gtg gac gtg atc gag tcc tgg gac gag tgg cct gac atc gag	480
Ser Val Val Asp Val Ile Glu Ser Trp Asp Glu Trp Pro Asp Ile Glu	
145 150 155 160	

taa	483
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<210> 11
 <211> 160
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

<400> 11

Met Ala Ser Lys Val Tyr Asp Pro Glu Gln Arg Lys Arg Met Ile Thr
 1 5 10 15

Gly Pro Gln Trp Trp Ala Arg Cys Lys Gln Met Asn Val Leu Asp Ser
 20 25 30

Phe Ile Asn Tyr Tyr Asp Ser Glu Lys His Ala Glu Asn Ala Val Ile
 35 40 45

Phe Leu His Gly Asn Ala Ala Ser Ser Tyr Leu Trp Arg His Val Val
 50 55 60

Pro His Ile Glu Pro Val Ala Arg Cys Ile Ile Pro Asp Leu Ile Gly
 65 70 75 80

Met Gly Lys Ser Gly Lys Ser Gly Asn Gly Ser Tyr Arg Leu Leu Asp
 85 90 95

His Tyr Lys Tyr Leu Thr Ala Trp Phe Glu Leu Leu Asn Leu Pro Lys
 100 105 110

Lys Ile Ile Phe Val Gly His Asp Trp Gly Ala Ala Leu Ala Phe His
 115 120 125

Tyr Ser Tyr Glu His Gln Asp Lys Ile Lys Ala Ile Val His Ala Glu
 130 135 140

Ser Val Val Asp Val Ile Glu Ser Trp Asp Glu Trp Pro Asp Ile Glu
 145 150 155 160

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<210> 12
<211> 480
<212> DNA
<213> Artificial

<220>
<223> synthetic construct; RLuc(F1) with C124A mutation, initiating
      "atg" removed, and stop codon at end

<220>
<221> CDS
<222> (1)..(480)

<400> 12
gct tcc aag gtg tac gac ccc gag caa cgc aaa cgc atg atc act ggg      48
Ala Ser Lys Val Tyr Asp Pro Glu Gln Arg Lys Arg Met Ile Thr Gly
1          5          10          15

cct cag tgg tgg gct cgc tgc aag caa atg aac gtg ctg gac tcc ttc      96
Pro Gln Trp Trp Ala Arg Cys Lys Gln Met Asn Val Leu Asp Ser Phe
          20          25          30

atc aac tac tat gat tcc gag aag cac gcc gag aac gcc gtg att ttt     144
Ile Asn Tyr Tyr Asp Ser Glu Lys His Ala Glu Asn Ala Val Ile Phe
          35          40          45

ctg cat ggt aac gct gcc tcc agc tac ctg tgg agg cac gtc gtg cct     192
Leu His Gly Asn Ala Ala Ser Ser Tyr Leu Trp Arg His Val Val Pro
          50          55          60

cac atc gag ccc gtg gct aga tgc atc atc cct gat ctg atc gga atg     240
His Ile Glu Pro Val Ala Arg Cys Ile Ile Pro Asp Leu Ile Gly Met
65          70          75          80

ggt aag tcc ggc aag agc ggg aat ggc tca tat cgc ctc ctg gat cac     288
Gly Lys Ser Gly Lys Ser Gly Asn Gly Ser Tyr Arg Leu Leu Asp His
          85          90          95

tac aag tac ctc acc gct tgg ttc gag ctg ctg aac ctt cca aag aaa     336
Tyr Lys Tyr Leu Thr Ala Trp Phe Glu Leu Leu Asn Leu Pro Lys Lys
          100          105          110

atc atc ttt gtg ggc cac gac tgg ggg gct gct ctg gcc ttt cac tac     384
Ile Ile Phe Val Gly His Asp Trp Gly Ala Ala Leu Ala Phe His Tyr
          115          120          125

tcc tac gag cac caa gac aag atc aag gcc atc gtc cat gct gag agt     432
Ser Tyr Glu His Gln Asp Lys Ile Lys Ala Ile Val His Ala Glu Ser
          130          135          140

gtc gtg gac gtg atc gag tcc tgg gac gag tgg cct gac atc gag taa     480
Val Val Asp Val Ile Glu Ser Trp Asp Glu Trp Pro Asp Ile Glu
145          150          155

```

<210> 13
 <211> 159
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

<400> 13

Ala Ser Lys Val Tyr Asp Pro Glu Gln Arg Lys Arg Met Ile Thr Gly
 1 5 10 15

Pro Gln Trp Trp Ala Arg Cys Lys Gln Met Asn Val Leu Asp Ser Phe
 20 25 30

Ile Asn Tyr Tyr Asp Ser Glu Lys His Ala Glu Asn Ala Val Ile Phe
 35 40 45

Leu His Gly Asn Ala Ala Ser Ser Tyr Leu Trp Arg His Val Val Pro
 50 55 60

His Ile Glu Pro Val Ala Arg Cys Ile Ile Pro Asp Leu Ile Gly Met
 65 70 75 80

Gly Lys Ser Gly Lys Ser Gly Asn Gly Ser Tyr Arg Leu Leu Asp His
 85 90 95

Tyr Lys Tyr Leu Thr Ala Trp Phe Glu Leu Leu Asn Leu Pro Lys Lys
 100 105 110

Ile Ile Phe Val Gly His Asp Trp Gly Ala Ala Leu Ala Phe His Tyr
 115 120 125

Ser Tyr Glu His Gln Asp Lys Ile Lys Ala Ile Val His Ala Glu Ser
 130 135 140

Val Val Asp Val Ile Glu Ser Trp Asp Glu Trp Pro Asp Ile Glu
 145 150 155

<210> 14
 <211> 477
 <212> DNA
 <213> Artificial

<220>
 <223> synthetic construct; YFP(F1) with added stop codon at end

<220>
 <221> CDS
 <222> (1)..(477)
 <223> YFP(F1) corresponds to a.a. 1-158 of the full length EYFP

<400> 14
 atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144
 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192
 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60

ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240
 Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
 65 70 75 80

cag cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288
 Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336
 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc 384
 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac 432
 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140

aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag taa 477
 Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln
 145 150 155

<210> 15
 <211> 158
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

<400> 15

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60

Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
 65 70 75 80

Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln
 145 150 155

<210> 16
 <211> 474
 <212> DNA
 <213> Artificial

<220>

<223> synthetic construct; YFP(F1) with stop codon added at end and
 initial "atg" (or Met) removed

<220>

<221> CDS

<222> (1)..(474)

<223> YFP(F1) corresponds to a.a. 1-158 of the full length EYFP

<400> 16

gtg	agc	aag	ggc	gag	gag	ctg	ttc	acc	ggg	gtg	gtg	ccc	atc	ctg	gtc	48
Val	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	Leu	Val	
1			5						10					15		

gag	ctg	gac	ggc	gac	gta	aac	ggc	cac	aag	ttc	agc	gtg	tcc	ggc	gag	96
Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	His	Lys	Phe	Ser	Val	Ser	Gly	Glu	
			20					25					30			

ggc	gag	ggc	gat	gcc	acc	tac	ggc	aag	ctg	acc	ctg	aag	ttc	atc	tgc	144
Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile	Cys	
			35				40					45				

acc	acc	ggc	aag	ctg	ccc	gtg	ccc	tgg	ccc	acc	ctc	gtg	acc	acc	ttc	192
Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr	Phe	
			50			55					60					

ggc	tac	ggc	ctg	cag	tgc	ttc	gcc	cgc	tac	ccc	gac	cac	atg	aag	cag	240
Gly	Tyr	Gly	Leu	Gln	Cys	Phe	Ala	Arg	Tyr	Pro	Asp	His	Met	Lys	Gln	
65				70				75						80		

cac	gac	ttc	ttc	aag	tcc	gcc	atg	ccc	gaa	ggc	tac	gtc	cag	gag	cgc	288
His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	Arg	
				85				90					95			

acc	atc	ttc	ttc	aag	gac	gac	ggc	aac	tac	aag	acc	cgc	gcc	gag	gtg	336
Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	Val	
			100				105						110			

aag	ttc	gag	ggc	gac	acc	ctg	gtg	aac	cgc	atc	gag	ctg	aag	ggc	atc	384
Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	Ile	
		115				120						125				

gac	ttc	aag	gag	gac	ggc	aac	atc	ctg	ggg	cac	aag	ctg	gag	tac	aac	432
Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	Asn	
		130				135					140					

tac	aac	agc	cac	aac	gtc	tat	atc	atg	gcc	gac	aag	cag	taa			474
Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln				
145					150				155							

<210> 17
 <211> 157
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

<400> 17

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
 1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
 20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
 35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
 50 55 60

Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Gln
 65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln
 145 150 155

<210> 18
 <211> 249
 <212> DNA
 <213> Artificial

<220>
 <223> synthetic construct; YFP(F2) with added "atg" (or Met) at position 1 and stop codon at end

<220>
 <221> CDS
 <222> (1)..(249)
 <223> YFP(F2) corresponds to a.a. 159-239 of the full length EYFP

<400> 18
 atg aag aac ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag 48
 Met Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu
 1 5 10 15
 gac ggc agc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc 96
 Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile
 20 25 30
 ggc gac ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc tac cag 144
 Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln
 35 40 45
 tcc gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg 192
 Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu
 50 55 60
 ctg gag ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg 240
 Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu
 65 70 75 80
 tac aag taa 249
 Tyr Lys

<210> 19
 <211> 82
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

<400> 19

Met Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu
1 5 10 15

Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile
20 25 30

Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln
35 40 45

Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu
50 55 60

Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu
65 70 75 80

Tyr Lys

<210> 20

<211> 246

<212> DNA

<213> Artificial

<220>

<223> synthetic construct; YFP(F2) with added stop codon at end

<220>

<221> CDS

<222> (1)..(246)

<223> YFP(F2) corresponds to a.a. 159-239 of the full length EYFP

<400> 20

aag aac ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac 48
Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
1 5 10 15

ggc agc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc 96
Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly
20 25 30

gac ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc tac cag tcc 144
Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser
35 40 45

gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg 192
Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu
50 55 60

gag ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac 240
Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr
65 70 75 80

```
<210> 21
<211> 81
<212> PRT
<213> Artificial
```

<400> 21

Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly
20 25 30

Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu
50 55 60

Lys

<210> 22
 <211> 477
 <212> DNA
 <213> Artificial

<220>
 <223> synthetic construct; IFP(F1) with stop codon added at end

<220>
 <221> CDS
 <222> (1)..(477)
 <223> IFP(F1) corresponds to a F46L mutated form of SEYFP(F1)

<400> 22
 atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15
 gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30
 gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttg atc 144
 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile
 35 40 45
 tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192
 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60
 ctc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240
 Leu Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
 65 70 75 80
 cag cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288
 Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95
 cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336
 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110
 gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc 384
 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125
 atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac 432
 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140
 aac tac aac agc cac aac gtc tat atc acg gcc gac aag cag taa 477
 Asn Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln
 145 150 155

<210> 23
 <211> 158
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

<400> 23

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile
 35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60

Leu Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
 65 70 75 80

Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln
 145 150 155

<210> 24
 <211> 474
 <212> DNA
 <213> Artificial

<220>
 <223> synthetic construct; IFP(F1) with initiating "atg" (or Met) removed and stop codon added at end

<220>
 <221> CDS
 <222> (1)..(474)
 <223> IFP(F1) corresponds to a F46L mutated form of SEYFP(F1)

<400> 24
 gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc 48
 Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
 1 5 10 15
 gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96
 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
 20 25 30
 ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttg atc tgc 144
 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile Cys
 35 40 45
 acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctc 192
 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
 50 55 60
 ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag cag 240
 Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Gln
 65 70 75 80
 cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288
 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 85 90 95
 acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg 336
 Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 100 105 110
 aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc 384
 Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 115 120 125
 gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac 432
 Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 130 135 140
 tac aac agc cac aac gtc tat atc acg gcc gac aag cag taa 474
 Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln
 145 150 155

<210> 25
 <211> 157
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

<400> 25

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
 1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
 20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Leu Ile Cys
 35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
 50 55 60

Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Gln
 65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln
 145 150 155

<210> 26
 <211> 249
 <212> DNA
 <213> Artificial

<220>
 <223> synthetic construct; IFP(F2) with added "atg" (or Met) at position 1 and a stop codon at the end

<220>
 <221> CDS
 <222> (1)..(249)
 <223> IFP(F2) corresponds to a V163A, S175G mutated form of YFP(F2)

<400> 26
 atg aag aac ggc atc aag gcg aac ttc aag atc cgc cac aac atc gag 48
 Met Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu
 1 5 10 15
 gac ggc ggc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc 96
 Asp Gly Gly Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile
 20 25 30
 ggc gac ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc tac cag 144
 Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln
 35 40 45
 tcc gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg 192
 Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu
 50 55 60
 ctg gag ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg 240
 Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu
 65 70 75 80
 tac aag taa 249
 Tyr Lys

<210> 27
 <211> 82
 <212> PRT
 <213> Artificial

<220>
 <223> Synthetic Construct

<400> 27
 Met Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu
 1 5 10 15

Asp Gly Gly Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile
20 25 30

Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln
35 40 45

Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu
50 55 60

Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu
65 70 75 80

Tyr Lys

<210> 28
<211> 246
<212> DNA
<213> Artificial

<220>
<223> synthetic construct; IFP(F2) with an added stop codon at the end

<220>
<221> CDS
<222> (1)..(246)
<223> IFP(F2) corresponds to a V163A, S175G mutated form of YFP(F2)

<400> 28
aag aac ggc atc aag gcg aac ttc aag atc cgc cac aac atc gag gac 48
Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp
1 5 10 15
ggc ggc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc 96
Gly Gly Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly
20 25 30
gac ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc tac cag tcc 144
Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser
35 40 45
gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg 192
Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu
50 55 60
gag ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac 240
Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr
65 70 75 80
aag taa 246
Lys

<210> 29
<211> 81
<212> PRT
<213> Artificial

<220>
<223> Synthetic Construct

<400> 29

Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp
1 5 10 15

Gly Gly Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly
20 25 30

Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser
35 40 45

Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu
50 55 60

Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr
65 70 75 80

Lys

<210> 30
<211> 15
<212> PRT
<213> Artificial

<220>
<223> synthetic construct, a flexible linker

<400> 30

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10 15

<210> 31
<211> 5
<212> PRT
<213> Artificial

<220>

<223> synthetic construct, "5-mer" building block for flexible linkers

<400> 31

Gly Gly Gly Gly Ser
1 5

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re of the Application of

Stephen Michnick et al

Serial Number: *unassigned*

Filed: February 5, 2004

For: PROTEIN FRAGMENT
COMPLEMENTATION ASSAYS
FOR HIGH THROUGHPUT AND
HIGH CONTENT SCREENING

Group Art Unit: *to be assigned*
Examiner: *to be assigned*

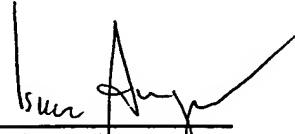
STATEMENT UNDER 37 C.F.R. 1.821(f)

Hon. Commissioner of Patents
and Trademarks
Alexandria, VA 22313

Dear Sir:

In regards to the above-captioned patent application and sequence listing (both paper copy and computer readable format) filed simultaneously herewith, Applicants' agent attests that the information recorded in the computer readable form is identical to the written sequence listing as required under 37 C.F.R. 1.821(f).

Respectfully submitted,


Isaac Angres
Reg. No. 29,765

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